

## Figure 2

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	Sequence ID #	
NRG1_alpha	1	TGTSHLVKAEKEKTCVNGGECFMVKDLSNPSRYLCKCQPGFTGARTENVPMKV
NRG1_beta	2	TGTSHLVKAEKEKTCVNGGECFMVKDLSNPSRYLCKCPNEFTGDRQCQNYVMASF
NRG2_alpha	3	SWSGHARKCNETAKSYCVNGGVYIEGINQLS--CKCPNGFFGQRCLEKLPRL
NRG2_beta	4	SWSGHARKCNETAKSYCVNGGVYIEGINQLS--CKCPVGYTGDRCCQCFAMVNF
NRG3	5	ERSEHFKPCRDKDLAYCLNDGECFVIETLTGSHK-HCRCKEGYQGVRCDDQLPKTD
NRG4	6	MPTDHEEPCGSPSHKSFCLNGGLCYVIPTIP--SP-FCRCVENYTGARCEEVFLPGS
EGF	7	SVRNSDSECLSHDGYCLHDGVCMYEALDKYA--CNCVGYIGERCQYRDLKWW
TGF_alpha	8	AWSHFNDCPDSHTQCFH-GTCRFLVQEDKPA--CVCHSGWVGARCEHADLLAV
Betacellulin	9	KRKGHFSRCPKQYKHYCIK-GRCRFVVAEQTPS--CVCDEGYIGARCERVDLFYL
Amphiregulin	10	RNRKKKNPCNAEFQNFICIH-GECKYIEHLEAVT--CKCQQEYFGERCGEKSMTK
HB-EGF	11	GLGKKRDPCLRKYKDFCIH-GECKYVKELRAP--CICHPGYHGERCHGLSLPVE
Epiregulin	12	VAQVSITKCSSDMNGYCLH-GQCIYLVDMSQNY--CRCEVGYTGVRCEHFFLTVH
Epigen	13	VALKFSPCLCEDHNSYCIN-GACAFHHELKQAI--CRCFTGYTGQRCEHLTTSY
		* :*: * * * * *

Figure 3

	Sequence ID #	4/8
<b>HUMAN</b>		
NRG1_alpha	14	
NRG1_beta	15	
Translated genomic locus	73, 128	
		<p>           &lt;----- Exon A -----&gt;----- Exon B -----&gt;            TGTSHLVKCAEKEKTFVNGGECFWKDLSPESRYLCKCPQFTGARCCTENVPKVVQ...            TGTSHLVKCAEKEKTFVNGGECFWKDLSPESRYLCKCPNEFTGDRCCQNYVMASFY...            TGTSHLVKCAEKEKTFVNGGECFWKDLSPESRYLCK*         </p>
NRG2_alpha	16	
NRG2_beta	17	
Translated genomic locus	74, 129	
		<p>           SWSGHARKCNETAKSYCVNGGVCYVIEGINQLS...CKCPNGFFGQRCLEKPLRLY...            SWSGHARKCNETAKSYCVNGGVCYVIEGINQLS...CKCPVGYTGDRCCQFAMVNFY...            SWSGHARKCNETAKSYCVNGGVCYVIEGINQLS...CK*         </p>
NRG3	18	
Translated genomic locus	75, 130	
		<p>           ERSEHFKPCRDKDLAYCLNDGECFVETLTGSH-KHCRCKEGYQGVRCQ-FLPKTD...            ERSEHFKPCRDKDLAYCLNDGECFVETLTGSH-KHCR*         </p>
NRG4	19	
Translated genomic locus	76, 131	
		<p>           MPTDHEEPCGSPSHKSFCLNGGLCYVITIPSPF...CRGVENYTGARCEEVFLPGSS...            MPTDHEEPCGSPSHKSFCLNGGLCYVITIPSPF...CR*         </p>
EGF	20	
Translated genomic locus	77, 132	
		<p>           SVRNSDSEPLSHDGYCLHDGVCVMYIEALDKYA---CNCWVGYIGERCQYRDLKWWE...            SVRNSDSEPLSHDGYCLHDGVCVMYIEALDKYA---CK*         </p>
TGF_alpha	21	
Translated genomic locus	78, 133	
		<p>           AVVSHFNDPDSHTQCFH-GTCRELVOEDKPA---GVCHSGYVGARCEHADLLAVV...            AVVSHFNDPDSHTQCFH-GTCRELVOEDKPA---GV*         </p>
Betacellulin	22	
Translated genomic locus	79, 134	
		<p>           KRKGHSRCPKQYKHVCK-KRCRFVVAEQTPS---CVCDEGYIGARCEVDFLFLR...            KRKGHSRCPKQYKHVCK-KRCRFVVAEQTPS---CV*         </p>

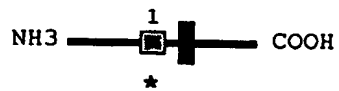
Figure 4

Amphiregulin Translated genomic locus	NRKKKNPCNAEFONFCIH-GECKYIEHLEAVT-CKCQOEYFGERGGEKSMKTHS.... NRKKKNPCNAEFONFCIH-GECKYIEHLEAVT-CK*	23 80, 135
HB-EGF Translated genomic locus	GLGKKRDPCLRYKDFCIH-GECKYVKELRAPST-CHPHGYHGERCHGLSLPVEN.... GLGKKRDPCLRYKDFCIH-GECKYVKELRAPST-CM*	24 81, 136
Epiregulin Translated genomic locus	VAQVSITKCSSDMNGYCLH-GOCKYLVDMSONY-RCCEVGYTGVRCEHFFLTVHQ.... VAQVSITKCSSDMNGYCLH-GOCKYLVDMSONY-CR*	25 82, 137
Epigen(Mouse) Trans. mouse genomic locus Trans. human genomic locus	VALKFSHPCEEDHNSYCIN-GACAFHHELKQAI-RCRFTGYTGQRCHEHLTLTSYA.... VALKFSHPCEEDHNSYCIN-GACAFHHELKQAI-CR* VALKFSHLCLEDHNSYCIN-GACAFHHELEKAI-CR*	26 83, 138 84, 139

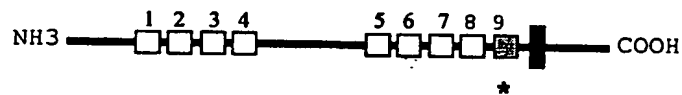
Figure 4 (continued)

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## i) TGF-alpha



## ii) Epidermal Growth Factor



## iii) Notch 1

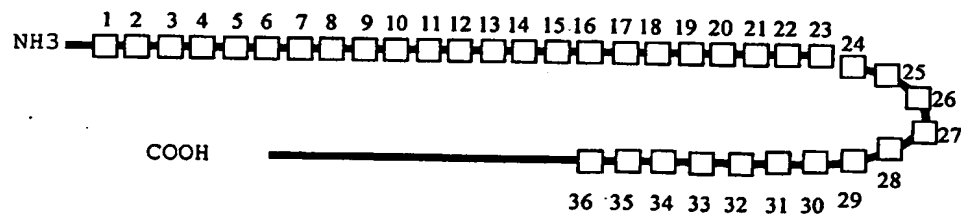


Figure 5A

i) TGF alpha		Sequence ID #
EGF DOMAIN NUMBER	SEQUENCE	
1. EGF_47_82 *	QDDSHLQDQD-HGDI-GRKLVQEDRPAGVCHSG--YVGAR--C	72
ii) EPIDERMAL GROWTH FACTOR		
EGF DOMAIN NUMBER	SEQUENCE	Sequence ID #
1. EGF_318_354	CKLR-KGNC--STVGGQDL--QSHLCMAEGYALSRRDKYC	27
2. EGF_360_395	CAFW-NHCC--PIGGKNTF--GSYCTCPVGVNHPDGKRG	28
3. EGF_401_436	CPRN-VSEC--SHDCVITS--EGRLCRGREGSMERDQKIC	29
4. EGF_439-476	CSSPDNGCCS--QVCMPESE--VSTECDEFPQDQDDEKSC	30
5. EGF_745_780	EDYQFNCCG--EHKCKGL--GTAWCSCREGEMKASDQKIC	31
6. EGF_835_868	CAEV--COS-LYARQISEG--EDATCOCKG--FAGEGKIC	32
7. EGF_874_910	CEMG-VPVQPPASSKGINIL--GSVWRGSEG--YQCDGPHC	33
8. EGF_916_951	EQLC-VHSEGLNAS-GINTE--CGYTCMCAGR--LSEPGKIC	34
9. EGF_976_1012 *	CELSHDSGL--HDGVCMTALDKKACN-CVVG--YIGER--C	35
iii) Notch1		
EGF DOMAIN NUMBER	SEQUENCE	Sequence ID #
1. EGF_24_57	CSQ-----PGETCLNGGKCEAANGTE-----ACVCG-GAFVGPRC	36
2. EGF_63_98	CHS-----TPCKNAGICH-VWDRRGVADYACSCA-EGESGPIG	37
3. EGF_106_138	CLT-----NPCRNGGTCD-TITITL--FLYKCRCP-PCWSGKSC	38
4. EGF_144_175	CAS-----NPCANGGCG--LP-LEASYTQHCP-PSEHGPIG	39
5. EGF_182_215	CCQ-----KPLCRHGGTCHNEVGSY--FRGVCR-ATHHTGNC	40
6. EGF_222_254	CSRSP-----CONGGTCRETCDV--THHCAGL-PGFTGQNC	41
7. EGF_261_292	CEGNN-----CKNGGACV-DGVN--LYNCPGP-PEWTGQYC	42
8. EGF_299_332	EQL-----MPNACONGCTCHNTHGGY--NEVCV-NCWTGSDG	43
9. EGF_339_370	CAS-----ACGTHGATCH-DRVA--SYXCEGP-HGRTGLLC	44
10. EGF_376_409	CHS-----NPENEGSNCD-TNPPV-NGKATCTCP-SGYTGPGC	45
11. EGF_416_449	CSL-----GANPCEHAGKCINTLGSE-----ECQCL-QGYTGPRC	46
12. EGF_456_487	CVS-----NPGONDATOL-DOIG--LPGCMCM-PGYEGVHC	47
13. EGF_494_525	CAS-----SECLHNGROL-DGIN--LPGCEGP-TGFTGHLG	48
14. EGF_532_563	CAS-----TPCKNAGKCL-DGPN--LYTCEVCP-EGYTGTIC	49
15. EGF_570_600	CDPDP-----CHYG-SCK-DGVA--LSTGLCR-PGYTGHHG	50
16. EGF_607_638	ESS-----OPCRNRTGTCQ-DPDN--LYTCEVCP-KGFTGPNL	51
17. EGF_645_675	CAS-----SEC-DSGTGL-DGID--GYECACE-PGYTCSMC	52
18. EGF_682_713	CAG-----NPGHNGTCL--ED-GINGETCRCP-EGYHDPIC	53
19. EGF_720_750	CNS-----NEGVHGARD--SLN--GYKCDGD-PGWSGTNC	54
20. EGF_757_788	CPS-----NPGVNGGTCK-D-MTS--GIVCTCR-EGESGPNC	55
21. EGF_795_826	CAS-----NPGANKGIC--IDD--VAGYKONCL-LPYTGATC	56
22. EGF_833_867	CAR-----SPCRNGGECR-OSPD-YESE-ESCVGPTAGAKGQTC	57
23. EGF_874_905	CVL-----SPCRHGASCO-NTHG--XYKCHCO-ACYSGRNG	58
24. EGF_912_943	CRPNP-----CHNGGSCT-DGIN--TAFCDCL-PGFRGTFC	59
25. EGF_950_981	CAS--DP-----CRNGANCT-DCVD--SYTCTCP-ACFSGIHC	60
26. EGF_988_1019	CHSS-----CFNGGTCTV-DGIN--SFTCLCP-PGFTGSYC	61
27. EGF_1026_1057	CDS-----RPFOLLGCTGQ-DG--RGHHRCTCP-OCYTGPNC	62
28. EGF_1064_1095	CDS-----SPCKNGGKCV-OT--HTQYRCECP-SGWTGPIY	63
29. EGF_1102_1143	CEVVAQPRGVDVARLCQHGGLCV-DAGN--THHCRCQ-AGYTGSYC	64
30. EGF_1150_1181	CSR-----SECONGATCT-DYIC--GYSCV-AGYHGUNC	65
31. EGF_1188_1219	CLS-----NPGCONGCTOL-DLPN--LYKCSOP-RCTGVHC	66
32. EGF_1226_1265	ENPEVDPVRS--PKCNNGTCTV-DOVG--GYSGTCTP-PGTVGERG	67
33. EGF_1272_1305	CLS-----NPGDARTON-CVOR--VNDHCECP-AGHTERRC	68
34. EGF_1312_1346	CKG-----KPGKNGGTCA-VASN-TARGETICKOP-AGFEGATC	69
35. EGF_1353_1384	Q-----CSLRCLNGCTCTSGPRSP--TCECP-GPFTGPEG	70
36. EGF_1392_1426	CLV-----CGNPEXNOGTCEPTSESPF--YRCLCP-AKFNGLIC	71

Figure 5B

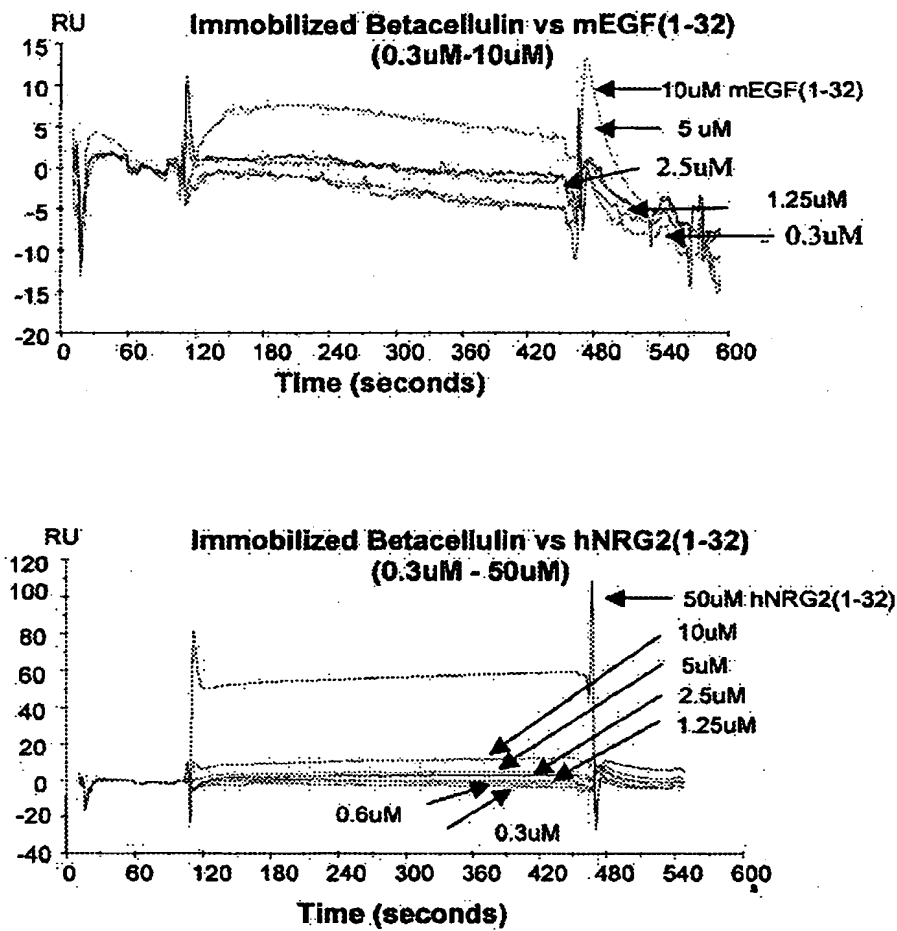


Figure 6